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GenCore version 4.5

OM protein - protein search, using sw model
Run on: May 29, 2002, 11:38:48 ; Search time 21.33 Seconds
(without alignments)
2914.665 Million cell updates/sec

Title: US-08-485-355B-50
Perfect score: 3374
Sequence: 1 MGDAVGAVASORPHNRGTRNV.....GKIAARVRAARRARRAAN 647

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2179	64	6	644 capsid protein - N
2	130	3	9	597 hypothetical prote
3	130	3	9	708 B75556 hypothetical prote
4	126	3	7	35701 Q0BEBB UL80 protein - hum
5	125.5	3	7	35705 T45025 mucin MUC5B trach
6	125	3	7	1269 A90267 proteinase related
7	123.5	3	7	2314 T28698 hypothetical prote
8	123	3	6	1209 S29605 probable pyrolysin
9	122	3	6	1582 AC1153 glycoprotein 350/2
10	121.5	3	6	907 adhesin homolog 1m
11	120	3	6	873 B75514 membrane antigen g
12	119.5	3	5	889 penicillin-binding
13	119	3	5	2271 T09055 protocadherin 6B -
14	119	3	5	1363 T43220 hypothetical prote
15	119	3	5	1993 AF1450 insulin-like grow
16	119	3	5	2809 T30213 probable peptide
17	118.5	3	5	3029 S76109 G-cadherin - sea u
18	117.5	3	5	609 hypothetical prote
19	117.5	3	5	884 S62518 conserved hypothet
20	117.5	3	5	355 E75489 titin, cardiac mus
21	117	3	5	26926 1 A97490 hypothetical prote
22	117	3	5	674 AE2217 hypothetical prote
23	116	3	4	859 E2217 hypothetical prote
24	115.5	3	4	3716 2 E70969 probable PPE prote
25	115	3	4	699 2 A8368 chitinase (EC 3.2.
26	115	3	4	3624 AD0835 large repetitive p
27	114.5	3	4	1419 2 T30531 agglutinin-like ad
28	114	3	4	710 1 Q0BE22 membrane antigen g
29	113.5	3	4	828 T12184 probable transcri
	113.5	3	4	781 1 VCPV19 coat protein VPL -

Query Match Score BB 2179

capsid protein - Nudaurelia omega virus
C.Species: Nudaurelia omega virus
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

30	113	3.3	4436	2	ET1086	hypothetical prote
31	112.5	3.3	604	2	AB4753	hypothetical prote
32	112	3.3	1090	2	S55077	cellulose 1,4-beta
33	112	3.3	1578	2	AD1512	peptidoglycan boun
34	111.5	3.3	604	2	T31042	hypothetical prote
35	111	3.3	1902	2	AB45764	lactocrepin (EC 3.4
36	110.5	3.3	505	2	S39962	endoglucanase - Er
37	110.5	3.3	677	2	ET5563	probable peptidyl-
38	109.5	3.3	792	2	F88656	protein F55b6.1 (1
39	109.5	3.2	1662	2	T18540	mfa protein precu
40	109	3.2	591	2	B87361	flagellar hook pro
41	109	3.2	86597		Cm711	hypothetical
42	109	3.2	766	2	F72027	conserved Hypothet
43	109	3.2	1302	2	T30191	multidrug resistan
44	108.5	3.2	642	2	B73428	laminarinase - The
45	108	3.2	424		T32434	Hypothetical prote

Db	406 INFFNLDAAITTAASNRSEVPLPPLPTFGQTAPNPKIESTLVKTLGSLVHSMRNPVQ	465	Qy	471 LTPASSFGAVSFNNPGYERTRDIDPYTGTRDSFDONMSAVAHRSLSHSCSIVTKTYQ	530
Db	466 LTPASSFGASIFNTFNGFDRNLIDCPFGGGIRDSLVDNMSTAVCHRSLSKCSIWIKYQG	525	Qy	531 WEGVTVNVPGEFAHAGLKNRKTLCADDATLRLTGIVYPAUDNFAAVASPAANMSS	590
Db	526 WEGVTVNVPGEFAHAGLKNRKTLCADDATLRLTGIVYPAUDNFAAVASPAANMSS	585	Qy	591 VLKSEATSSIKSYGETAVGAROGLAKLPLGLMSVPKIAARRRARARRARAN	647
Db	586 VLKSEATSSIKSYGETAVGAROGLAKLPLGLMSVPKIAARRRARARRARAN	642	Qy	588 -LSSLVLKSEATSSIKSYGE	606
RESULT	2		Db	499 GMAPTLLHQAGDITCSYGD	518
B7556	hypothetical protein - Deinococcus radiodurans		Qy	473 -PASSEFGAVSFNNPGYERTRDIDPYTGTRDSFDONMSAVAHRSLSHSCSIVTKTYQ	529
C;Species: Deinococcus radiodurans			Db	403 EFPQGAGPKFCGN-----YDAMT-TISQSSTLTATTSSIANGPVADT-	449
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000			Qy	530 GWGCVTNYN-TPQGQFAHAGLKNRKTLCADDATLRLTGIVYPATDNFAAVSAFAANM-	587
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Ventler, J.C.; Fraser, C.M.			Db	450 -----INITPGANYTREVLKDNDVAFSGPDSDR---YTCTINATTGSTIVMPTNS	498
Science 286, 1571-1577, 1999			Qy	588 -LSSLVLKSEATSSIKSYGE	606
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Reference number: A73250; MUID:2003896			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Accession: B7556			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Status: preliminary			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Molecule type: DNA			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Residues: 1-597 <WHI>			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Cross-references: GB:AE001876; GB:AB000513; NID:96457800; PIDN:AAF09732.1; PID:9645780			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Experimental source: strain R1			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
C;Genetics:			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Gene: DR0143			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
A;Map position: 1			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
Query Match 3.9%; Score 130; DB 2; Length 597;			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
Best Local Similarity 20.6%; Pred. No. 0.36; Mismatches 128; Conservative 67; Indels 172; Gaps 25;			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
Matches 128; Conservative 67; Indels 172; Gaps 25;			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
Qy 54 QDIAQSDANTIVPPANISSMPPER---NWAKGKIDDSDSIGWYKLDAGAT--- 105			Db	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533
Db 4 RDIVDSLPAQPGQMVWTSPPHQAVQCVNNSCGIISNSGMSLSTESSDGGATWPPA 63			Qy	106 ---ESARAVGEYSKIPDGIVKSVDAETE--TYNEECP--VVTDVSVPLDROWSLI 157	
Qy 106 ---ESARAVGEYSKIPDGIVKSVDAETE--TYNEECP--VVTDVSVPLDROWSLI 157			Db	64 PRGATORSVPGVNLIPACTCRSFDVILPRACTYKVNIPANRITSQGNDAGQASITA 123	
Db 64 PRGATORSVPGVNLIPACTCRSFDVILPRACTYKVNIPANRITSQGNDAGQASITA 123			Qy	158 FSPMPERRY-----VAVVANENKENSLDV-WNDLEWLNNIADWRVV 200	
Qy 158 FSPMPERRY-----VAVVANENKENSLDV-WNDLEWLNNIADWRVV 200			Db	124 FAQPTVTKAYSPKPSILGDGKATSTLTITLNNSSSPAVSLTAPLTIDNIG--NGLEITGVTT 181	
Db 124 FAQPTVTKAYSPKPSILGDGKATSTLTITLNNSSSPAVSLTAPLTIDNIG--NGLEITGVTT 181			Qy	201 DSQWINTNDTYYVRRVRLR---TVDVDPTELVRLVTSYDRTYKATCERNAMP 255	
Qy 201 DSQWINTNDTYYVRRVRLR---TVDVDPTELVRLVTSYDRTYKATCERNAMP 255			Db	182 SCGTTATPSGTTTYPSCATLNHGTCITATVHSATAG-----SYP 222	
Db 182 SCGTTATPSGTTTYPSCATLNHGTCITATVHSATAG-----SYP 222			Qy	269 ALIPTSLPODYDSEAYAL-HTLFARSSAAALAFWAGLPOGGTAPAGTPAWEQASSGG 327	
Qy 269 ALIPTSLPODYDSEAYAL-HTLFARSSAAALAFWAGLPOGGTAPAGTPAWEQASSGG 327			Db	319 AESPPSLSPSEPREAASMSPLSAANPATA-----PPGATVAGASA--VSS- 364	
Db 319 AESPPSLSPSEPREAASMSPLSAANPATA-----PPGATVAGASA--VSS- 364			Qy	328 YLWWRHNGTTFAGSVSYLVPGEFALERYDPNDGSWIDFASAGDTWTFROYAVDEVWTN 387	
Qy 328 YLWWRHNGTTFAGSVSYLVPGEFALERYDPNDGSWIDFASAGDTWTFROYAVDEVWTN 387			Db	365 -LAPWPHDCVYLPRDAFFSSL----- 383	
Db 365 -LAPWPHDCVYLPRDAFFSSL----- 383			Qy	298 AAIAAFVWAGLPGQGTAPAGTAPANEQASGGYLWLRWRHNGTTEPGSVSYLVPGEFALERYD 357	
Qy 298 AAIAAFVWAGLPGQGTAPAGTAPANEQASGGYLWLRWRHNGTTEPGSVSYLVPGEFALERYD 357			Db	283 AA-----TSGALSLSDLPPGMSFNSVT 305	
Db 283 AA-----TSGALSLSDLPPGMSFNSVT 305			Qy	388 NPAGGGSAPFTVVRVPSNAYINTVFRNTILETRPSSRRLPMP--PAPFGQTWANNPK 445	
Qy 388 NPAGGGSAPFTVVRVPSNAYINTVFRNTILETRPSSRRLPMP--PAPFGQTWANNPK 445			Db	359 PNDGSMWDFASAGDTWTFROYAVDEVWTN 416	
Db 359 PNDGSMWDFASAGDTWTFROYAVDEVWTN 416			Qy	306 TTGGGSRGTRPAGAT----GRWDWTPSPPLAAGOSLTFWTVNANTVANGATLN 360	
Db 306 TTGGGSRGTRPAGAT----GRWDWTPSPPLAAGOSLTFWTVNANTVANGATLN 360			Qy	417 LLTRPSSRRLPMPAD-FGOTVANNPKIESSLKETLGCVLVHSKMRNPWFOLT-- 472	
Qy 417 LLTRPSSRRLPMPAD-FGOTVANNPKIESSLKETLGCVLVHSKMRNPWFOLT-- 472			Db	361 YASVGGGDPDVTPGATCTGSCASDPTV-----NITQTLRK 402	
Db 361 YASVGGGDPDVTPGATCTGSCASDPTV-----NITQTLRK 402			Qy	496 -----YTGTRDSEFDOM-----STAVAHRSLSHSCSIVTKTYQWEG	533

RESULT 4

Db 480 EPPSGWERYDGGHGRGQSOOKHRHGGHHNKRKETAAASSSSSDEDLSPFGCAEHGRAR 539
 C Species: Homo sapiens (man)
 C Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C Accession: T45025
 A Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat R. Desseyne, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
 A Reference number: z22899; MUID:97166151
 A Status: preliminary; translated from GB/EMBL/DBJ
 A Molecule type: DNA
 A Residues: 1-3570 <DSS>
 A Cross-references: EMBL:Z72496; NID:91834502; PIDN:CAA96577.1; PID:91834503
 A Experimental source: placenta
 C Genetics: A:Gene: MUC5B

Query Match 3.7%; Score 126; DB 2; Length 3570;
 Best Local Similarity 22.3%; Pred. No. 11; Matches 94; Conservative 32; Mismatches 178; Indels 118; Gaps 14;

Qy 221 LRPTYDVPDPPTGGLVRLVRSDYFLTY---KATICEANMPMTLQDGFWIGGYALTTSLP 276
 Db 643 LSTATTPATTAIPSSLLGTWTWILSQTTIPMATM-----ATPSSTP 689
 Qy 277 QDVSEAYALHLT-----FARRSSAALAFWAGLPGQGTAPACTAWEO 322
 Db 690 E-----TVHHTSVLTATTGTATGATSVATATSTPCTAHTTKVLTTTGTTATPSSP 742
 Qy 323 ASGGYLTWHRHQTTFAGSVSYVLPGEFALERYDPNGSWTDFASAGDTYFROAVDE 382
 Db 743 GRARTLPWM-TSTTTPTRGSTVTPSSI-----PGTHMPTVLT 784
 Qy 383 VVVTNNIAGGGSAPTFTVVRPDSNAYINTVFRNTLLETRPSSRRLELPMPADFGQTVAN 442
 Db 785 TTVATGSMATPSSQTGSGTPSLTTATTITATGSTINPSTPGTIPPV-LTTAT 842
 Qy 443 NPKIEQSLKETLGCVLYHSKMRNPVHOLTPRSSGAVSFNNPGYBTRDADPDYGIRDS 502
 Db 843 TRATSS-----TVPSSALGTT-----HTPPVFN----- 867
 Qy 503 FDQNMSTAVAHRSLSH-----CSIVTKTQGWEGYTVNWPFGQFAH----AGLKN 552
 Db 868 -----TTATTHGRSLSPSSPHVTCTANTISATGIGLGTHTIPSTGTSHTPATGTOH 922
 Qy 553 EBTICLADDLATRIGYPA---TDNEAAVYSAFAA-----NMSSVLSKEATSSIIK 602
 Db 923 SPPALSSPHPSRTTESPPSPCTTPTCHTATAPSRTATAPSRTATPSKTRTSTLPSQPSAPIT 982
 Qy 603 SV 604
 Db 983 TV 984

RESULT 5

Db 20267 proteinase related protein [imported] - Sulfolobus solfataricus
 C Species: Sulfolobus solfataricus
 C Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

RESULT 6

T28698 hypothetical protein - Streptomyces coelicolor
 C Species: Streptomyces coelicolor
 C Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C Accession: T28698
 R. Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1999
 A Reference number: 220512
 A Accession: T28698
 A Status: preliminary; translated from GB/EMBL/DBJ
 A Molecule type: DNA
 A Residues: 1-2314 <PAR>
 A Cross-references: EMBL:AL023496; NID:e1292348; PID:e1292365; PIDN:CAA18915.1
 C:Accession: A90267
 R. She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch Jong, I.; Jeffries, A.C.; Koza, C.J.; Medina, N.; Peng, X.; Thi-Noc, H.P.; Redder arrett, R.A.; Regan, M.A.; Seneca, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A:Description: Sulfolobus solfataricus complete genome.
 A:Reference number: A99139
 A:Accession: A90267
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1269 <KUR>
 A:Cross-references: GB:AE006641; NID:918314328; PIDN:AAK41392.1; GSPPB:GN00155
 C:Genetics:
 A:Gene: SSO1141

Query Match 3.7%; Score 125.5; DB 2; Length 1269;
 Best Local Similarity 19.6%; Pred. No. 2.4; Matches 98; Conservative 69; Mismatches 181; Indels 153; Gaps 27;

Qy 18 RNVRVSANTVTYNGRNRRRNGROVSPPDNFTAAQDLAQSDANTVTPANITSSMPER 77
 Db 584 ORILVITANITYPNG-----SPVQ--TGFEFKALIENYLGNLNTFLNTVNSLKL 629
 Qy 78 RWWAKGKDLDSDSIGWYKFLDPAGATESARAVGYESKPDGLVFKFSVDAEIRBY-- 134
 Db 630 -WT-GSGVLENKASGFLFVY--YGSSDLRGIGYETPSGYYTIFNYTTFPVYV 684
 Qy 135 -NEECPVVTDVS--VPLDGROWSSIFSFMFRTAYVAFAN---VENNEMSLDVNDL 186
 Db 685 GNAELGILTSLNSYFQAPIGVNITLNIYSYNITNAYTFVILSPIKGIVGVLDPDL 744
 Qy 187 IEWLNNAIDWRVYWDSEOW--INFNTD--TYYVIRV----- 187 LRP 223
 Db 745 -----SIGDLILIAEGRNAGFDAFTINGVYMOFLFILPQVVVEPGSVSPGQHITEGSIIP 799
 Qy 224 TYDVPDT--EGLVRYSDYRUYTKITC-----EAMPTFLDQGFWIGGYAIPPTSL 275
 Db 800 PVNLPSMFODALQT---NITAKLVSSNGVVINENAPIP-LSPNGIYFG--YLVIPKT 852
 Qy 276 PQ-YDV-----SEAYALHLTFFARPSSAAL---AFWAGLHQ 309
 Db 853 PSGLYNVLFLAAYYSTNTNTIRGFYQGQIVSNQATISVKSNTAFEGQTVETANTN 912
 Qy 310 GCTA-----PAG-----TPAWQOASSCGYLWWRHNGT--TFPAGS 342
 Db 913 GNEIKFGMFSAVVYSSLSFNNTISSIEIPLWNPKIG--EWEGNFTLPSAISAG 969
 Qy 343 VSYVLPGEFALEYDPNGSWTDEASAGDTYFROAVDEVWVNTPAGGSAPIFTVY 402
 Db 970 LTYLAGOGYF----- 1009
 Qy 403 PPSNAVINTVFRNTLLETRPS 423
 Db 1010 LPYTLFTN---QTLDKTLPS 1026

Query Match 3.7%; Score 125; DB 2; Length 2314;
 Best Local Similarity 21.0%; Pred. No. 6.5; Mismatches 217; Conservatve 77; Indels 260; Gaps 36; Matches 157;

A;Gene: PAB1252
 C;Keywords: hydrolase

C;Genetics:
 A;Status: Preliminary
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C;Accession: C75015
 A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAH50561.1; PID:9545907
 A;Experimental source: strain Orsay

Query Match 3.7%; Score 125; DB 2; Length 2314;
 Best Local Similarity 21.0%; Pred. No. 6.5; Mismatches 217; Conservatve 77; Indels 260; Gaps 36; Matches 157; Conservatve 77; Mismatches 260; Gaps 36;

Qy 35 ORRRT--GROVSPPDNFTRAQDIAQSLDANTTFFPANISSMMPEFRWAKGKIDLDSDI 92
 Db 979 ERARHVLAQDASPPTGLMAHDALRSVADLTIDEGGYAVLOAEDPDRMEGP-SLVKEA- 1036
 Qy 93 GWYKYKLDDAGATESARAVGEYSKIPDGIV-- 104
 Db 1037 --YVSDGLGGVYVEGAWE--QYDLDFFGGVAPRSVSVRYANSQAAAEPSSVUDIHAGD-- 1090
 Qy 135 NEECRVVDTDSVP----- 158
 Db 1091 -ADGPVVATVSLPGTGGWYQYTTVRAAVSDPQALKASSATFWFHAPSROW-VSNFDWY 1148
 Qy 159 -----SFPHERTAYAVAVANVEN--EMSDUVNDLIEMLN--LADMRYVWSEQ 204
 Db 1149 QFSPEAAPSSPPIITLATLTANTSTGDGSPLKVGSGVFENVTNGAWAER----- 1201
 Qy 205 WINFTNDTYTIVRVLRLPTYDPDPTEGVLVRVSDYRITYK-----AITE---- 251
 Db 1202 -----DIDLGDADTVTSYDPR-----RAASDHIELRFGAKDQPTAVVPLDVTG 1250
 Qy 252 -----ANHAPTLPDQFWIGGQ--YALPNTSLPQDVSEBAYA-LHTLFAROSSAA--- 298
 Db 1251 SGWCTVASTSVRLDPDVFGTQVIAVVFSS-TQTDQPYVANVHSLTLTROADAPVFD 1309
 Qy 299 ALARVWAGLPGQGSTPAPAGTPAWIQQASSGGL-----TWRHNGTTFPGSVSULPECFAL 353
 Db 1310 ATAP----- 1340
 Qy 354 ERTDPNDGSWTDPASAGQVTFRQVAVDEWV--NNNA--GGSAPIFTVVRPPSNAYT 409
 Db 1341 -----YDGAWL-----GD-VDEGDSPKNVTLYNNARCCTGSAV----- 1378
 Qy 410 NTWFRNTLETRSSRRLPMPADFGOTVANKPTEQSLKETLGVLVLSKMRNEWF 469
 Db 1379 -QYLDSDFPDAGTPTVPLVY-GSSWSGGTISLTBLERAITGTHAVHLRITNAD 1435
 Qy 470 QLTP-ASSPGAVERNPNPGYERTDLDPTGIRDSFDQNMSTAVAHFRSLSHSCSIIVRTY 528
 Db 1436 SSMPVANIGQVAFDRVERPAQD----- 1467
 Qy 529 QGREGVNT-----VNTPPGQF-----AHAGLKEETILCLADDLADR-LTGVYPATNEA 577
 Db 1468 EQEGLSEDADRYGTIDFGVFRRELTAARDLIGTTEADOLEADLRTSRLT----- 1517
 Qy 578 AASFAANML-----SSULKSEATSSIKSUGFTEAVSAQASSLAKLFCLL 623
 Db 1518 -----LAANOLVPLPRLLESVATASALADERYTDAWSKAFTTALTAKTALADETAD 1572
 Qy 624 MSVPGKIAARVARRA---RRRARA 646
 Db 1573 RTTTERVALDRRSSUTTKRRTVPA 1598

RESULT 7
 C75015 probable pyrolysin (EC 3.4.-.-) homolog PAB1252 [similarity] - Pyrococcus abyssi (strain C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C;Accession: C75015
 A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAH50561.1; PID:9545907
 A;Experimental source: strain Orsay
 A;Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru

RESULT 8
 A;Accession: C75015
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-1204 <KAW>
 A;Cross-references: GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAH50561.1; PID:9545907
 A;Experimental source: strain Orsay

Qy 510 AVAFRSLHSCSIVTIVQYQHEGVINNTNPGQFAHAGLIKNEELCLADDLTRLT- 567
 Db 862 LKITNVTRVEGGKSIELT---YNATS---GYYTKVTLENGAVTLLVVTATDELNNVT 913
 Qy 510 AVAFRSLHSCSIVTIVQYQHEGVINNTNPGQFAHAGLIKNEELCLADDLTRLT- 567
 Db 914 ARVHF-VVSANAKVTPVIVEN---TIVT-----VGVGNATITVTDWVNTTS 960
 Qy 568 -GYY---PATDNFAAVSAFA-ANMILSSVIKSEATSSIKSUGFTEAVGAQSG 615
 Db 961 ECYIEVKVPPWN---APAIIVNSTAEDVVKGANATLVAGWNWVTTKEVG 1011

Qy 510 AVAFRSLHSCSIVTIVQYQHEGVINNTNPGQFAHAGLIKNEELCLADDLTRLT- 567
 Db 914 ARVHF-VVSANAKVTPVIVEN---TIVT-----VGVGNATITVTDWVNTTS 960
 Qy 568 -GYY---PATDNFAAVSAFA-ANMILSSVIKSEATSSIKSUGFTEAVGAQSG 615
 Db 961 ECYIEVKVPPWN---APAIIVNSTAEDVVKGANATLVAGWNWVTTKEVG 1011

Qy 510 AVAFRSLHSCSIVTIVQYQHEGVINNTNPGQFAHAGLIKNEELCLADDLTRLT- 567
 Db 914 ARVHF-VVSANAKVTPVIVEN---TIVT-----VGVGNATITVTDWVNTTS 960
 Qy 568 -GYY---PATDNFAAVSAFA-ANMILSSVIKSEATSSIKSUGFTEAVGAQSG 615
 Db 961 ECYIEVKVPPWN---APAIIVNSTAEDVVKGANATLVAGWNWVTTKEVG 1011

Submitted to the EMBL Data Library, October 1992
 A; Description: Sequences of the membrane proteins gp 350/220 and p140 of Epstein-Barr virus
 A; Reference number: S29605
 A; Accession: S29605
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-886 <KLE>
 A; Cross-references: EMBL:X67776; NID:959163; PIDN:CAA47986.1; PID:959164
 C; Family: Epstein-Barr virus membrane antigen gp350
 C; Keywords: glycoprotein

Query Match

Score 3.6%; Score 123; DB 2; Length 886;

Best Local Similarity 20.3%; Pred. No. 2; Mismatches 269; Indels 206; Gaps 29;
 Matches 138; Conservative 66; Mismatches 269; Indels 206; Gaps 29;

D.; Jones, L.M.; Karst, U.
 Science 274, 849-852, 2001.
 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maitournam, A.;
 Ok, C.; Schlueter, T.; Sarnes, N.; Tieriez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla,
 A; Title: Comparative genomics of Listeria species.
 A; Reference number: AB1077; MUID:21537279; PMID:11675659
 A; Accession: ACI153
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-1582 <GLA>
 A; Cross-references: GB:NC_003210; PIDN:CAAC98705.1; PID:916410016; GSFDB:GN00177
 A; Experimental source: strain EGD-e
 C; Genetics: C; Genomics:
 A; Gene: lmo0627

Query Match

Score 3.6%; Score 122; DB 2; Length 1582;

Best Local Similarity 19.6%; Pred. No. 5.9; Mismatches 247; Indels 160; Gaps 35;
 Matches 122; Conservative 92; Mismatches 247; Indels 160; Gaps 35;

D.; Jones, L.M.; Karst, U.
 Science 274, 849-852, 2001.
 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maitournam, A.;
 Ok, C.; Schlueter, T.; Sarnes, N.; Tieriez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla,
 A; Title: Comparative genomics of Listeria species.
 A; Reference number: AB1077; MUID:21537279; PMID:11675659
 A; Accession: ACI153
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-1582 <GLA>
 A; Cross-references: GB:NC_003210; PIDN:CAAC98705.1; PID:916410016; GSFDB:GN00177
 A; Experimental source: strain EGD-e
 C; Genetics: C; Genomics:
 A; Gene: lmo0627

Qy 48 NFTAAQDQLAQSDANTVTPANISMPEFRWAKGKIDLDSDSIGWFKYLLDPAGES 107
 Db 169 NTAVVR--RQGLD--VTPRLSLPISAOQNSFS---VKTEIMLG---NEID---IEC 211
 Qy 108 ARAVGEYSKIPDGLYKFVPSVDAEIRE-----IYNEECPVYTVDVSPVLDGROWSLISFE 160
 Db 212 IMDGEISIQVLPQGDNRKFNITCGYSHVPSGGILSTSPVAT--PIPGTGAYASLRTPR 269
 Qy 161 PMFR----TAYVAVANVENKEMSD----VNDL-----EWLNNLADWRVVDSE 203
 Db 270 PVSRELGNNSITLVYFVGNGPCKASGDCYCIOSNTVSDEIFASQDMPTNTDITVGDN- 328
 Qy 204 QWINFTNDTYVYRIRVLRLPTDVDPTEGLVRLTVSDYRLTYKAITCCEAMPLVLDQGFN 263
 Db 329 -----ATYSPVHTE-----IGGOYALTPM-----DANSPNVVTAFW 352
 Qy 264 ----- 273
 Db 353 AWPNNETDFKCKWLTSGPSCENISGAFASNRTFDITVSLGLTAPKLITRATNA 412
 Qy 274 -----SFLQYDSEAYAHLTHLFARSSAAALAFWAGLPGQGTAAAGTPEWQAS 324
 Db 413 TTTKHKVIFSRAPESTTSPNLTGFAADNT-----TGLPSSTHVTNLTA---PAS 463
 Qy 325 SGGYLAWRHNCTTFPGSVSVLPGCFALRYPDNQG-----SWTDEASAGDVTFRQ 377
 Db 464 TGPVSTADVISPTPAGTTGASP---VTPSPSPRONGTESKAPDMTSPTSAVTPTPNA 520
 Qy 378 VAVDEVVVT---NNPAGGGSAPFTVRYPPSNAYNT-----VRNLTLETRPS 423
 Db 521 TSPTPAVITPPNATSPTIGTSPTSAVTPPTPNATSPTAVTTPNATIPTLGKTSPT 580
 Qy 424 SRKELPMPMPADFGQVANNKIEPLKELGCVLHKMRNPYFOLTPASSRCAVSFN 483
 Db 581 S-AVTPTPNTSPVGETSP---QANTTNHHTL-----GTSSTPVTSPPKNATSAVTG 632
 Qy 484 NFGYEVTRDLDYDTGIR-DSPDNQNSTAVAHFRSLSHSCSIVTKTYQGMWEGVINTPFG 542
 Db 633 Q-HNTSSSTSMSLRPSSSETLSPSTS-DNSTSHMLPLTSAHPTGGENTQV-TPAS 688
 Qy 543 QFAHAGLKLNEEILCLADDIATRLTCVYPAT-----DNAFAAVSAFAANMMLSSLVKE 595
 Db 689 TSTH-----HYSTSSPAPRGTSQASGPGNSSTSKPGEVNVTKGTPKN 734
 Qy 596 ATSSIIKSVGENAVGAQS 614
 Db 735 ATSPQAPSGQKTAIVPVT 753

RESULT 9

ACI153 adhesin homolog lmo0627 [imported] - Listeria monocytogenes (strain EGD-e)
 C; Species: Listeria monocytogenes
 C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
 C; Accession: ACI153
 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.

RESULT 10

QBE21 membrane antigen gp350 - human herpesvirus 4 (strain B95-8)
 C; Species: human herpesvirus 4, Epstein-Barr virus
 C; Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 28-Jul-2000
 C; Accession: AA3040; S33008; S33009; AA3762
 R; Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
 Mol. Biol. Med. 1, 21-45, 1983

A;Title: Sequence analysis of the 17,166 bp ECOLI fragment C of B95-8 Epstein-Barr virus	Db	687	HMPLLTSAAHPGGENITQV-TPASITH-----HVSISSPARPGTQS 731
A;Reference number: K93065; NID:65035113			
A;Accession: A43042			
A;Molecule type: DNA			
A;Residues: 1-907 <BAND>			
A;Cross-references: GB:v01555; GB:J02070; GB:K01729; GB:K01730; GB:V01554; GB:X00498; GE			
R;Parrell, P.J.			
A;Submitted to the EMBL Data Library, March 1988			
A;Reference number: S32973			
A;Accession: S33008			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-907 <FA2>			
A;Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24855_1; PID:91334869			
R;Baird, R.; Bankier, A.T.; Braggan, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H			
Nature 310, 207-211, 1984			
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.			
A;Reference number: A03794; NID:84270567			
A;Contents: annotation: protein coding region			
C;superfamily: Epstein-Barr virus membrane antigen gp350			
Query Match 3 6%; Score 121.5; DB 1; Length 907; Best Local Similarity 19.6%; Pred. No. 2.7; Mismatches 138; Conservative 66; Mismatches 266; Indels 233; Gaps 28; Matches 138; Status: preliminary			
Qy 48 NFTAAQDQAQSDANTVFPANISSMPFERNWAKGKIDDSIGWYKLDPPAGTES 107			
Db 169 NTIAVWR-AQGLD--VVLPLSLPTSDADSNS---VKTEMLG--NEID---IEC 211			
Qy 108 ARAVGEYSKIPDGIVKFSVDAETRE-----TYNEECVVTVDYSPVLOGRSLSIFSF 160			
Db 212 IMEGEISQVLPGDKNKFNITCSGKESHVSGGILSTSVAT--PIPGCYAKSRLTR 269			
Qy 161 PMF-----TAVAVAVENKENKNSLD-----VNDLIT---EWLNLLADWVYVSE 203			
Db 270 PVSRFLGNKNSILVYFVSGNGPKASGGDYCIOSNITVFSDELPSQDMPTWTDITYVGDN- 328			
Qy 204 QWINFINDTIYVIRVLRPTVDPDTCGLVRIVSDVLYTKRITCEANAMPTVQGW 263			
Db 329 -----ATVSPVMVSE-----DANSRPTVTAW 352			
Qy 264 -----IGQYALIPT----- 273			
Db 353 AWPNTEIDFKCKWTLSGTPSGCENISGAFASFNRTEDITVSGLGTAPEKLITRATA 412			
Qy 274 -----SLPQDVSEYAHULTFAPPSAALAFWAGLQGGTVPAGTPAWEQAS 324			
Db 413 TTTHTHKVTSKAPESTTSTPLNTTGADPNT-----TGLPSSTHVTPLNTA-PAS 463			
Qy 325 SGGLITWHRNGTTPAGSISVILEPREGFALERIDNGS-----TDFASAGDV 373			
Db 464 TGPVTVSTADVTSPTPAGTSPGASP-----VTPSPSPDNGTESKAPMTSSPVTP 516			
Qy 374 TFRQAVADVVVT-----NNPAGGGSAPTEVVRVPSNATNTVFR 414			
Db 517 TPNTATSPPFPAVTPTPNTATSPTRAVTTPPNATSPPTLGLTSPSAVTPNTATSP 576			
Qy 415 N-----TLETRPSSRRELPPPADGQCTVANNPKLQLQSLLKETGCG 458			
Db 577 TSPTSAVTPTPNTATSPTRGKTSPS-AVTTPTPNTAT-GPTVGETSP-QANATHTLG- 631			
Qy 459 LVIHKMRKRVFQFLPASSEGAVERNNPGQERDPLDPYGIROSFDQNMSTAVHFRS 518			
Db 632 --GTSPPPPVTSQPKNATSAVTGQ-- HNITSSTSSNLSRQSSNPELSPSPSDNSIS 686			
Qy 519 HCSIVTKVYQGREGVNTNTPPGQFAHGLKNEELGLADDLATRUTGVYPAT---- 573			
RESULT 11			
B75514 penicillin-binding protein 1 - Deinococcus radiodurans (strain R1)			
C;Species: Deinococcus radiodurans			
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000			
C;Accession: B75514			
R;White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Podson, R.J.; H			
'M.; Shen, M.; Yamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.M.			
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.			
Science 286, 1511-1577, 1999			
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.			
A;Reference number: A7520; NID:20036896			
A;Accession: B75514			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-873 <WHI>			
A;Cross-references: GB:AE001907; GB:AE000513; NID:96458162; PID:AAF10059_1; PID:9645			
C;Genetics:			
A;Experimental source: strain R1			
C;Genetics:			
A;Gene: DR479			
A;Map position: 1			
Query Match 3 6%; Score 120; DB 2; Length 873; Best Local Similarity 26.0%; Pred. No. 3.2; Mismatches 72; Conservative 19; Mismatches 104; Indels 82; Gaps 16; Matches 72; Status: preliminary			
Qy 208 FTNDTYYIVRIVLR-----PTVDVDPDPM-----EGLVRTSYDRL 243			
Db 545 FANGGUYAYASAVERMEDPOGKVKKRKPDPVGKRYWDKRYAWLGIDMIRGVNDISAYQ- 603			
Qy 244 TYKATCCEANMPTVQDFGFWTQGQVLTPTSLPQDVSEYALVHTLFAR-PRSSAALA 301			
Db 604 --GGATRARI-----DGWQVGGKIGT-----MDVKD-----LWFAGVYPLTSGA- 642			
Qy 302 FWVAGLIPQGSTAPA-----GTPAWEQASSGGYLTWRHNGTTEPAGSV-----SYVLPSEG 350			
Db 643 -WVSKOEGGTLPWSVAYSGEVPTPW-QAATAGALAGRETATFIPPGIVYRTYRNMA 700			
Qy 351 FALEYRDP-----NDGSWTDFAASAGTVTFRVAVADE-VVVTNNPAGGSAP-----T 397			
Db 701 FLTERNAQDPVRHDS---RRATXATPVAATAEPPQPATTGASRSPAPLRRRTT 756			
Qy 398 FTVRVPSPNSAVNTVFRNTLLETTRSSRRLPLMPMA 434			
Db 757 LPRQISPRRALPS---RTCRPRRPLSPPPRRPRPGA 789			
RESULT 12			
T09055 protocadherin 68 - human			
C;Species: Homo sapiens (man)			
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999			
C;Accession: T09055			
R;Jin, P.; Xu, H.; Israel, D.			
R;Submitted to the EMBL Data Library, October 1997.			
A;Reference number: 21650			
A;Accession: T09055			
A;Status: preliminary; translated from GB/EMBL/DDJB			
A;Molecule type: mRNA			
A;Residues: 1-889 <JIN>			
A;Cross-references: EMBL:AF029343; NID:92599501; PID:92599502			
C;Genetics:			
A;Gene: PCH68			

Query Match 3.5%; Score 119.5; DB 2; Length 889;
Best Local Similarity 20.4%; Pred. No. 3.6;
Matches 144; Conservative 92; Mismatches 250; Indels 219; Gaps 36;

Qy 32 RNRNRRRTGROWSPPDNTAAQDIAQSLDANTVTPANITSSMPERNWAKG----- 83
Db 97 RHNAKQQLSLEVFANDKEICMKIKEIQDINDNAPSFSQDXLDTSENAAPGTRPLTS 156
Qy 84 -KIDLDSDSTGWWYFKVLDPAQATE-SARAVGEYSKIPDGVLKFSDAETRETYNECPW 141
Db 157 HDPPDAGENGRLYLLJTRDDHGLFLGVSKSRGDTKPELVIQKALD--REQQNHHTLV 213
Qy 142 TDVSVPILDGROWWSLSIFSFPMERTAYAVAVENKEMS- LDVNNDIEMLNLA DWRYV 199
Db 214 T-ALDGG------PPRATVOINVKVDSI:SDNSPVFEAPSYLVEPLPNTFLGTW 262
Qy 200 VDEQOMINTN-----DTY---YVRIRVLRLPTYDVPDPTEGLVRTS--DY---- 241
Db 263 ID---LNATDADEGEVGEVLYSFSSYVPPDRY-REFLSI-DPKTGLIRVKGNLD 316
Qy 242 --.-----RLTYKAITECNAMEPTFLDQGFWMGGQYALTPTSFLPOYDVE 282
Db 317 LEIDVQARDLGPNLIPAHCKVTKLIDRNADNPST--GP-----VSVRGALSE 363
Qy 283 AVALHLTEFARPSAAALAFW--AG-----LPQGTTAPGTPANEQASSGGYL 330
Db 364 A-----APGTVTALVRVTDQKNGNQLCRVLGGGGGGG----- 401
Qy 331 WRHNGTTPAGSVSYVLPGEFLERYKDPMGSWTDEASAGDTVTFRQV--AVDEVVTN 387
Db 402 ---GLGGPGSGSVPERLEENY-----DNFTY-----VVTDRPMDESETQDBYN 442
Qy 388 NPGGGSAP---TFTVRV-----PP---SNAVNTVFRNLTETRPSSRRLPELMP 433
Db 443 VARDGGSPPLNSTKSPAIIKILDNDNPPTKGVLQVHENNI-----PG 488
Qy 434 ADPGQVANNERIEQ-----SLLKETLGYLVHKMR-NPWFOLTPASSFGAVSN 486
Db 489 DXLGSVLAQDPDGLGQNTGTVSYSILPSHIGDVSIYTVSVNP---TNGATYALRSFN-- 541
Qy 487 YERTROLPDYTGIROS-----FDQNMSTAVAHFRSLSHSCSIVTVQYQREG- 533
Db 542 FEQTAKAFEFKVLA KDSGAPAHLESNATVRYTVLVDVNDAPVTVLPTLQNDTAELQVPRNA 601
Qy 534 ---VTVNNTPFQFAHAGLKL-----NEELCIADDIATRLTGVPAMDN-----F 576
Db 602 GLGYLVSTVRA LSPGESGRLTVEIVDGDDHREIDFSSGEIKTLHPFWEDVTPVVEL 661
Qy 577 AA VAVSAFAANM LSSV KSE TSIT KSVG FET AVGA QAO SGIA KLPG 621
Db 662 VVKVTDHGKPTLSAVAK----LIIRSVS---GSPEGVPRVNG 697

RESULT 13

f90073 hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F90073
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Oji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Accession number: A89758; MUID:21311952; PMID:11418146
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <KUR>
A;Cross-references: GB:BA000018; PID:913702612; PIDN:BAB43752.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA2447

Query Match 3.5%; Score 119.5; DB 2; Length 2271;
Best Local Similarity 18.9%; Pred. No. 15;
Matches 147; Conservative 107; Mismatches 233; Indels 289; Gaps 37;

Qy 22 VSANTVWN-----GRRNRRRTGQRVSPPDNTAAQDIAQSLDANTVTPANITSSMPERNWAKG----- 70
Db 254 VTANTTIVKNDNLKQYMTSGNATDQSITQVTLTQDAY-----QKGATLGR 303
Qy 71 ISSMPERNWAKGKDLD-----DSIGWYK----- 97
Db 304 IDSNKSFH--FSGKVNGLNKYEGHNGGIGDGFASPVGWIGETGLNGA AVGIGGLSNAFG 361
Qy 98 -----YLD PAGATESARAVGEVSKI----- 126
Db 362 FKLDTYHNTSKRPNKAKANADPSNYAGGAFAGFAVFTDSYGVATTYSSSTADNAKLN 421
Qy 163 -----FRT-AYVAVANVENKENSIDVNDL-----EWLNLA DWRYVYDSEQ----- 204
Db 477 GATNLOQVQFCFETVESA TQV RYV DNTGKDIIPP KIYSGNVDQVWITDNOOSALTAK 536
Qy 205 WINFTN-DTYYVIRVRLRPTYDVPDPTEGLVRTYDYLTYKAITECNAMEPTFLDQG 263
Db 537 GINYTISVSDSSY-----ASTYN--DTNKTVMTNAGOSVTVYFTDVKA PTV TGVNQTE 587
Qy 264 IGGQVALTPTSLPQYDVS EAYALHQLTFLARPSSAA LA FWAGL P QG-----GTAPACT 317
Db 588 VG--KTMNMPVPUVLT TTDNGTGT VNTV T-----GLPSGLSYDSATNSIIGT 630
Qy 318 P-----AWEQASGGYL TW RHN-GTF PAGS SYVLP BG-FALER YD----- 358
Db 631 PTKIGOSTVTVSTQDANKRSTTTTINVWDTAP-----VTPIGDQSEEVSPISPK 685
Qy 359 -----NDGSWTFDASAGDTVTFRQVAVDEVVVTNNPAGGSSAPTR-----TVR VPPSNAY 408
Db 686 IATQDNGSN-----AVTIN V TGLPSGLTFDSTNTISGPTNIG 724
Qy 409 TNT-----VERNTLLET PSSRRLPELMPADFGFOTVANPKTQ 448
Db 725 TSTISIVSTDAGNKTTTFRYEVTRNSMSDSVSTGSO-----SQSVSTKADSQ 777
Qy 449 SLKETLGYLVHSKMRNPVFO LTPASSFGAVSN-NP3YERTROLPDYTGIRSDQDM 507
Db 778 SASTPSGSIVS-----TSASTSRSV SLSV SASKSLS-----TSESVS SST 825
Qy 508 STAVA HFRSLSHSCS-ITV KHYQWBGV TNNTPFQFAHAGL KNEE----- 555
Db 826 STSLVNSQSVSSSMSGSVSKSTSLSDISNSNS-----TEKSESLSSTSLSLR 876
Qy 556 LCLLADDLATRUTGVPATDIFAAVVAFAANMLSSVLSKPSATSSTIK--SVGTA 608
Db 877 TSLSDSLSMSLSTSLSKSQSLSTSISGSS-----TSASLSSTSNAISTSTSLS 929

RESULT 14

T43220 insulin-like growth factor-1 receptor - common lancelet
N;Alternate names: insulin-like peptide receptor
C;Species: Branchiostoma lanceolatum (common lancelet)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T43220
R;Paslimborough, M.; Chan, S.J.; Steiner, D.F.
Mol. Endocrinol. 10, 857-866, 1996
A;Title: Structure and expression of the insulin-like peptide receptor from amphioxus
A;Reference number: z22346; MUID:96408719
A;Accession: T43220
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-1363 <PAS>
 A;Cross-references: EMBL:S83394; NID:gi911771; PID:gi911772; PIDN:AAB50848.1
 C;Superfamily: insulin receptor; protein kinase homology
 C;Keywords: hormone receptor

Query Match 3.5%; Score 119; DB 2; Length 1363;
 Best Local Similarity 19.8%; Pred No. 7.6; Indels 260; gaps 38;
 Matches 99; Conservative 60; Mismatches 162; Gaps 23;
 Db 416 DWDWDRDITDEGKLFHHFKRKLCHVHLTMVKVLGPBHA-----ITD----- 458

Qy 79 NWAKGKIDDSDSGSWYFK-----YLDPAGATESARAVGEYSKIPDGIVKFSDA 128
 Db 459 -----TDISALTNGD-----AQCSRLE-----IE 480

Qy 189 WLNILNLADWRVWVSEQWVNFTNDTYYVIRVRLRPTYDVPDPEGLVPLVPSDRLTKA 248
 Db 481 EINISKDMIL----RWSEF-----RP---PDPRDLSTVTS YRET--- 514

Qy 249 TCEANNMPTLVDOGR-WIGGOYALIPTSLPQDYDVEAYALHTLFARPSAAAL---AEVW 304
 Db 515 -----EDQGJIDEYDQGACGNTEMKEFDVSPQTQAHITGLKPWTQYALVKT 565

Qy 305 AGURQGG-----TAPACTPANMQASSGGYLWHRHNTFPAGSVSVLP 348
 Db 566 AGAREGSGSAKSDDVYARTDADKPTHPDQVWVNSNSNNTLITWKPPNR--PNQNVTHIV 623

Qy 349 EGALERVDPNQDSWTDASAG---DIVTRQAVADVVNNPAGGSAPFTVRP 403
 Db 624 K-KRQOQDVAEAEQREYCKGGYKPHRPTQGLDGVNNEPNNSTGDTGIC---CECP 678

Qy 404 PS-----NAYNTNVRTLTETPSSRRLELPMPDAF-GQTVV--- 440
 Db 679 KSDDEIRTEEEAFOEFENFELHNWVHKRENETRAGRRLRELVPARFISSQNTVT 738

Qy 441 -----ANNKIESSLKETLGCVLHVSKRN--PVFELTPASSFGAVSFN 483
 Db 739 LPSTNRTVPPPTPPNPNFOLETTVWNEHM--VVLGLRHFSEXYLIEVIACNAADAVGCS 795

Qy 484 NPQYERTKLDLPTGIRSO 504
 Db 796 GSVELARTQAD----DSAD 811

RESULT 15

AFI450 probable peptidoglycan bound protein (LPXTG motif) lin0141 [imported] - Listeria innocua
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C;Accession: AFI450
 R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:2153729; PMID:11679969
 A;Accession: AFI450
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1993 <GLA>
 A;Cross-references: GB:AL592022; PIDN:CAC95374.1; PID:gi16412560; GSPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin0141

Query Match 3.5%; Score 119; DB 2; Length 1993;
 Best Local Similarity 19.3%; Pred No. 14; Indels 260; gaps 38;
 Matches 99; Conservative 60; Mismatches 162; Gaps 23;
 Db 1247 DASVA-----TAKTLTDGSVATVGGSTN----GKTRVTD-LTIALKDIFTEK 1291

Qy 63 NTWTFPANLISSAEPFRNWAKGKII---DLSDSIGWYFKYLDPGATESARAVGYESKIP 118
 Db 1292 STA-----PLVYTTANGVKAQKDELKIGATNFLEYKOAVVSE-AQAVTK---- 1336

Qy 119 DGLVKFSVDAETREIYNEECPVVTDVSYPLDGRQ-----WSLSITSFPMRTAVAVAN 172
 Db 1337 --AKTAFAFEEVYKGVNDAEDRTDV-VKVDQQLALKNGSNRGCTYPL-----TTELEKN 1389

Qy 173 VENKEMSDI-VVNDLTELWNMLAD-----WRYVVDSDSQWINFTNDYVYVRTRVL 222
 Db 1390 GKEVETVVDVKYEKDLTE-VRAHDSITVYGDNRRAADNEDSALNKKEGETLTFADEATG 1447

Qy 223 P-----TYDVPDPTECLVURPVSYDRYTYKATCENAMPTLVDOGFWI----- 264
 Db 1448 TVDTKAGEYPVYKTYKNTTKVITVVD-----DATEINAHSTDYTGTGDTWSAKDNFDS 1502

Qy 265 -----GQYALTPTSLPQDYDVEAYALHTLFARPSAAALAFWAGLPGGTAAGTPA 319
 Db 1503 AADRDGNEVALSKVTVNTVNTFAQGYTRPYITV-----YGGVSKHITY 1546

Qy 320 WEQASSGGYLWHRHNTFPAGSVSVLP EGFLERYDPNGSWT--DPSA---GDT 372
 Db 1547 VRENKKG---INAHNATLYVG-----DSWPAEDNDNAVDKDGNP 1583

Qy 373 VIFRQAVADEVY-VTNPAG-----GGAAPTAVRV----PPSNAYNTVFRNLE 419
 Db 1584 VEFSKVIVTETFVNNTKAGYIQLKTFDGA SKTVLTVKNIQTAVNAHNISTVYGETWE 1643

Qy 420 TR---PSRRRLPMPADGOTVA-NNPKLEQSLIKETGCYLHSK-----M 464
 Db 1644 AKDNFDSARNKD-----GETVAFADVEVGNVDMTVAQGTYVYKQFSKTIKVY 1695

Qy 465 RNPVFQLTTPASSE-----GAVSFNNIG--- 486
 Db 1696 KNPTAITAHDSSVYTGDNWSAKDNFDSAIDKAGKPVAYRBDTVEEDPTVLNTPGTYSV 1755

Qy 487 --YE-----RTRDLPYIG---IRDSDQ-----NMSTAVAH 513
 Db 1756 TYKYQGFSKQVWQITVKPQTKVESHOSTITAGASWNAKDFDSAIDKKGDKVLSDVYI 1815

Qy 514 PRSLSHSCSIVTKYQCGWEGVVNTPFGFAHAGLKNRERILCLADDLATRLTCVYPAT 573
 Db 1816 GRVNDGTPGTEITYR-YDGTSVSRVIVLHAKTIVNDSKL-----KINADWDRK 1866

Qy 574 DNFAAAYSFAANMLSLSVLSKSEATTSILKSYGETAV-----GAAQSGLAKL--PGU 623
 Db 1867 DNFRVAMSRDGSEIPMSKVKEGVN-TKAGKQVYTTIDPNEGTVDAKEEELSVATI 1925

Qy 624 MSVPGKIA 631
 Db 1926 EVVEGKVA 1933

Search completed: May 29, 2002, 11:40:28
 Job time: 100 sec